

Amendment and Response to Restriction Requirement
Application No. 10/822,254

Amendment to the claims:

Please cancel claims 6-13, 34-57.

Listing of Claims:

1 (Original). A polypeptide comprising the amino acid sequence of SEQ ID NO: 4; wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2); and wherein said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4.

2 (Original). The polypeptide according to claim 1, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 and SEQ ID NO: 12; wherein any one of said amino acid sequences optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 of said conservative amino acid substitutions.

3 (Original). The polypeptide according to claim 2, wherein said polypeptide optionally comprises 1, 2, or 3 of said conservative amino acid substitutions.

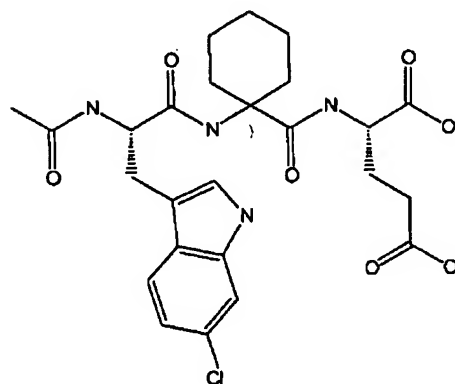
4 (Original). The polypeptide according to claim 3, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 and SEQ ID NO: 12.

5 (Original). The polypeptide according to claim 4, wherein said polypeptide consists of the amino acid sequence of selected from the group consisting of SEQ ID NO: 6 and SEQ ID NO: 10.

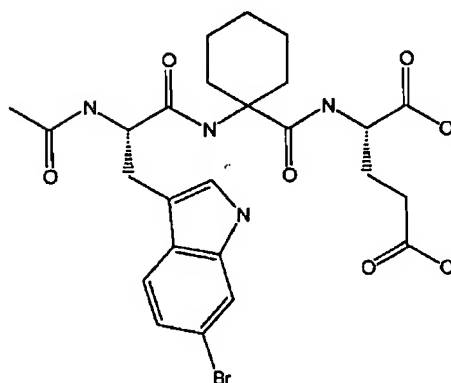
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6-13 (Cancel).

14 (Original). A compound selected from the group consisting of



and



15 (Original). A polypeptide-compound complex comprising the compound according to claim 14 and a polypeptide complexed to it, wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 4, wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2); and wherein said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10

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or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4.

16 (Original). A crystal comprising a polypeptide, wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 4, wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2); and wherein said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4.

17 (Original). The crystal according to claim 16, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 and SEQ ID NO: 12; wherein any one of said amino acid sequences optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 of said conservative amino acid substitutions.

18 (Original). The crystal according to claim 17, wherein said polypeptide optionally comprises 1, 2, or 3 of said conservative amino acid substitutions.

19 (Original). The crystal according to claim 18, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10 and SEQ ID NO: 12.

20 (Original). The crystal according to claim 19, wherein said polypeptide consists essentially of the amino acid sequence of selected from the group consisting of SEQ ID NO: 6 and SEQ ID NO: 10.

21 (Original). The crystal according to either of claims 16 or 20, wherein said crystal effectively diffracts X-rays to a resolution of greater than 5.0 Å.

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22 (Original). The crystal according to claim 21, wherein said crystal effectively diffracts X-rays to a resolution of greater than 2.5 Å.

23 (Original). The crystal according to claim 22, wherein said crystal effectively diffracts X-rays to a resolution of greater than 1.5 Å.

24 (Original). The crystal according to either of claims 16 or 20, wherein said polypeptide is complexed to a compound that binds said polypeptide and forms a polypeptide-compound complex.

25 (Original). The crystal according to claim 24, wherein said compound is selected from the group consisting of a peptide derived from p53, SCH549128, Ac-⁶⁰WAC₃cE and Ac-⁶⁰WAC₃cE.

26 (Original). The crystal according to claim 16, wherein said polypeptide consists of the amino acid of SEQ ID NO: 10 and said crystal has the structural coordinates as set forth in Table 3.

27 (Original). The crystal according to claim 16, wherein said polypeptide consists of the amino acid of SEQ ID NO: 6 and said crystal has the structural coordinates as set forth in Table 4.

28 (Original). A crystal comprising a polypeptide, wherein said polypeptide is characterized by structure coordinates comprising a root mean square deviation (RMSD) of conserved residue backbone atoms of less than about 2.0 Å when superimposed on backbone atoms described by structural coordinates of Table 3 or Table 4.

29 (Original). The crystal according to claim 28, wherein said RMSD is less than about 1.5 Å.

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30 (Original). The crystal according to claim 29, wherein said RMSD is less than about 1.0 Å.

31 (Original). The crystal according to claim 30, wherein said RMSD is less than about 0.5 Å.

32 (Original). The crystal according to claim 28, wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 4, wherein at least one of the seven variable positions of SEQ ID NO: 4 has an amino acid residue that differs from that of the corresponding wild-type Hdm2(17-125) amino acid sequence (SEQ ID NO: 2); and wherein said polypeptide optionally comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 conservative amino acid substitutions that are not at one of the seven variable positions of SEQ ID NO: 4.

33 (Original). The crystal according to claim 32, wherein said polypeptide comprises the amino acid sequence of SEQ ID NO: 8 or SEQ ID NO: 12.

34-57 (Cancel).

Remarks:

The claims that are now pending are claims 1-5 and 14-33. No new matter has been added to the application.

Election/Restriction. The Examiner has restricted the claims into 8 groups as follows:

Group I:	Claims 1-5, 14-33, 52 and 53.
Group II:	Claims 6-12.
Group III:	Claim 13.
Group IV:	Claims 34-39.
Group V:	Claims 40-47 and 55-57.
Group VI:	Claim 48.
Group VII:	Claims 49-51 and 54.

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Group VIII: Claims 55-57.

Applicants herein elect the claims of group I.